IFWO

RAW SEQUENCE LISTING   DATE: 09/16/2004
PATENT APPLICATION: US/10/774,176   TIME: 12:15:26

Input Set : **N:\Crf3\RULE60\10774176.raw**
Output Set: **N:\CRF4\09162004\J774176.raw**

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 1 <110> APPLICANT: CARROLL, MILES WILLIAM
 2        MYERS, KEVIN ALAN
 3 <120> TITLE OF INVENTION: POLYPEPTIDE
 4 <130> FILE REFERENCE: 078883/0120
 5 <140> CURRENT APPLICATION NUMBER: US/10/774,176
 6 <141> CURRENT FILING DATE: 2004-02-06
 7 <150> PRIOR APPLICATION NUMBER: US/09/533,798
 8 <151> PRIOR FILING DATE: 2000-03-24
 9 <150> PRIOR APPLICATION NUMBER: 60/126,187
10 <151> PRIOR FILING DATE: 1999-03-25
11 <150> PRIOR APPLICATION NUMBER: 60/126,188
12 <151> PRIOR FILING DATE: 1999-03-25
13 <150> PRIOR APPLICATION NUMBER: GB 9825303.2
14 <151> PRIOR FILING DATE: 1998-11-18
15 <150> PRIOR APPLICATION NUMBER: GB 9901739.4
16 <151> PRIOR FILING DATE: 1999-01-27
17 <150> PRIOR APPLICATION NUMBER: GB 9917995.4
18 <151> PRIOR FILING DATE: 1999-07-30
19 <160> NUMBER OF SEQ ID NOS: 27
20 <170> SOFTWARE: PatentIn version 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1263
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
26 <400> SEQUENCE: 1
27      atgcctgggg ggtgctcccg gggccccgcc gccggggacg ggcgtctgcg gctggcgcga      60
28      ctagcgctgg tactcctggg ctgggtctcc tcgtcttctc ccacctcctc ggcatcctcc     120
29      ttctcctcct cggcgccgtt cctggcttcc gccgtgtccg cccagccccc gctgccggac     180
30      cagtgccccg cgctgtgcga gtgctccgag gcagcgcgca cagtcaagtg cgttaaccgc     240
31      aatctgaccg aggtgcccac ggacctgccc gcctacgtgc gcaacctctt ccttaccggc     300
32      aaccagctgg ccgtgctccc tgccggcgcc ttcgcccgcc ggccgccgct ggcggagctg     360
33      gccgcgctca acctcagcgg cagccgcctg gacgaggtgc gcgcgggcgc cttcgagcat     420
34      ctgcccagcc tgcgccagct cgacctcagc cacaacccac tggccgacct cagtcccttc     480
35      gctttctcgg gcagcaatgc cagcgtctcg gcccccagtc ccttgtgga actgatcctg      540
36      aaccacatcg tgccccctga agatgagcgg cagaaccgga gcttcgaggg catggtggtg     600
37      gcggccctgc tggcgggccg tgcactgcag gggctccgcc gcttggagct ggccagcaac     660
38      cacttccttt acctgccgcg ggatgtgctg gcccaactgc ccagcctcag gcacctggac     720
39      ttaagtaata attcgctggt gagcctgacc tacgtgtcct ccgcaacct gacacatcta      780
40      gaaagcctcc acctggagga caatgccctc aaggtccttc acaatggcac cctggctgag     840
41      ttgcaaggtc taccccacat tagggttttc ctggacaaca atccctgggt ctgcgactgc     900
42      cacatggcag acatggtgac ctggctcaag gaaacagagg tagtgcaggg caaagaccgg     960
43      ctcacctgtg catatccgga aaaaatgagg aatcgggtcc tcttggaact caacagtgct    1020
44      gacctggact gtgacccgat tcttcccca tccctgcaaa cctcttatgt cttcctgggt    1080
```

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```
 45        attgttttag ccctgatagg cgctattttc ctcctggttt tgtatttgaa ccgcaagggg    1140
 46        ataaaaaagt ggatgcataa catcagagat gcctgcaggg atcacatgga agggtatcat    1200
 47        tacagatatg aaatcaatgc ggaccccaga ttaacaaacc tcagttctaa ctcggatgtc    1260
 48        tga                                                                  1263
 50 <210> SEQ ID NO: 2
 51 <211> LENGTH: 1281
 52 <212> TYPE: DNA
 53 <213> ORGANISM: Mus musculus
 54 <400> SEQUENCE: 2
 55        atgcctgggg cgggctcccg gggcccctcc gccggggacg gacggctgag gttggcaagg      60
 56        ctggcgctag tgctgctggg ttgggtctcc gcgtcggccc ccagctcttc ggtaccctcg     120
 57        tcttccacct ccccggcaga cttcctggcc tcggggtctg cgcagcctcc gccagccgag     180
 58        agatgccccg cggcgtgcga gtgctccgag gcggcgcgca cggttaagtg cgtgaaccgc     240
 59        aacctgctgg aggtgccggc ggatctaccg ccttacgtgc gcaacctttt ccttaccggc     300
 60        aaccagatga ccgtgctccc cgcgggcgcc ttcgcccgcc agccgccgct cgccgacctg     360
 61        gaggcgctca acctcagcgg caaccacctg aaggaggtgt gtgcaggtgc cttcgagcat     420
 62        ctgccgggtc tgcgccggct tgacctcagc cacaaccctc tcaccaacct cagcgccttc     480
 63        gtctttgcgg gcagcaacgc cagcgtctcg gcccccagcc ccctggagga gctgatcctg     540
 64        aatcacatcg tgccccctga ggatcagagg cagaacggga gcttcgaggg tatggtggcc     600
 65        ttcgaaggca tggtggcagc agctctgcgc tcaggccttg cactccgagg tcttacacgc     660
 66        ctggagctag ccagcaatca ctttcttttc ctgcctcggg acttactagc ccaactgccg     720
 67        agtctcagat acctggacct caggaacaat tccctggtga gcctgaccta cgcatccttc     780
 68        cgcaacctga cacacctcga aagcctccac ttggaggaca atgccctcaa ggtccttcac     840
 69        aactccacct tggctgagtg gcaaggcctg gctcatgtca aggtgttcct ggacaacaat     900
 70        ccctgggttt gcgactgcta catggctgac atggtggctt ggcttaaaga gacagaggtg     960
 71        gtgccagata aagccaggct tacctgcgca ttccccggaga agatgaggaa tcgtggcctc    1020
 72        ttagacctca acagctctga cctggactgt gacgctgtcc ttccccaatc cctgcagact    1080
 73        tcctatgtct tcctaggtat tgttttagct ctgataggcg ctattttcct cctcgttttg    1140
 74        tatttgaacc gtaaaggcat aaaaaagtgg atgcataaca tcagagatgc ctgcagggat    1200
 75        cacatggaag ggtatcatta cagatacgaa atcaatgcgg accccagatt aacaaatctt    1260
 76        agttccaact cggatgtctg a                                              1281
 78 <210> SEQ ID NO: 3
 79 <211> LENGTH: 901
 80 <212> TYPE: DNA
 81 <213> ORGANISM: Canis sp.
 82 <220> FEATURE:
 83 <221> NAME/KEY: modified_base
 84 <222> LOCATION: (66)
 85 <223> OTHER INFORMATION: a, c, g or t
 86 <221> NAME/KEY: modified_base
 87 <222> LOCATION: (145)
 88 <223> OTHER INFORMATION: a, c, g or t
```
W--> 89 **<221> modified_base**
```
 90 <222> LOCATION: (277)..(278)
 91 <223> OTHER INFORMATION: a, c, g or t
```
W--> 92 **<221> modified_base**
```
 93 <222> LOCATION: (287)
 94 <223> OTHER INFORMATION: a, c, g or t
```
W--> 95 **<221> modified_base**

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```
        96 <222> LOCATION: (353)
        97 <223> OTHER INFORMATION: a, c, g or t
W-->    98 <221> modified_base
        99 <222> LOCATION: (358)
       100 <223> OTHER INFORMATION: a, c, g or t
W-->   101 <221> modified_base
       102 <222> LOCATION: (428)..(429)
       103 <223> OTHER INFORMATION: a, c, g or t
W-->   104 <221> modified_base
       105 <222> LOCATION: (577)
       106 <223> OTHER INFORMATION: a, c, g or t
W-->   107 <221> modified_base
       108 <222> LOCATION: (580)
       109 <223> OTHER INFORMATION: a, c, g or t
W-->   110 <221> modified_base
       111 <222> LOCATION: (719)
       112 <223> OTHER INFORMATION: a, c, g or t
W-->   113 <221> modified_base
       114 <222> LOCATION: (788)
       115 <223> OTHER INFORMATION: a, c, g or t
W-->   116 <221> modified_base
       117 <222> LOCATION: (863)
       118 <223> OTHER INFORMATION: a, c, g or t
W-->   119 <221> modified_base
       120 <222> LOCATION: (868)
       121 <223> OTHER INFORMATION: a, c, g or t
W-->   122 <221> modified_base
       123 <222> LOCATION: (871)
       124 <223> OTHER INFORMATION: a, c, g or t
W-->   125 <400> 3
       126       atcgtgcccc ccgacgaccg gcggcagaac cggagcttcg aggtcatggt ggcggctgcc      60
W-->   127       vddrrnrsvm vaaactccga gcgggccgcg cgcttcgcgg gctgcagtgc ctggagctgg     120
       128       ccggcaaccg cttcragrar gcagnrctct acttgcctcg cgacgtcctg gcccagctac     180
       129       ccggcctccg gcacctggac ctgcgcyrdv agrhdraaca attccctggt gagcctcacc     240
       130       tacgtgtcct tccgcaacct gacgcacttg gagagcnnsv styvsrnths ctccacctgg     300
       131       aggacaacgc cctcaaggtc cttcacaacg ccaccctggc ggagctgcag hdnakvhnat     360
       132       aagcctgccc cacgtccggg tcttcctgga caacaacccc tgggtctgcg attgtcacat     420
       133       gshvrvdnnw vcdchmgcag acatggtggc ctggctcaag gagacagagg tggtgccggg     480
       134       caaagccggg ctcaccadmv awktvvgkag ttgtgcattc ccggagaaaa tgaggaatcg     540
       135       ggccctcttg gaactcaaca gctcccacct gcakmrnran sshgactgtg accctatcct     600
       136       ccctccatcc ctgcagactt cttatgtctt cctaggtatt gtcdcdstsy vgvttagccc     660
       137       tgataggcgc catcttccta ctggttttgt atttgaaccg caagggata aagagavynr     720
       138       kgkaagtgga tgcataacat cagagatgcc tgcagggatc acatggaagg gtatcactac     780
       139       agakwmhnrd acrdhmgyhy rtacgaaatc aatgcagacc ccaggttaac aaacctcagt     840
       140       tccaattcgg atgtctgaga aynadrtnss nsdvacagtc ggggacagac caaggacaac     900
       141       t                                                                    901
       143 <210> SEQ ID NO: 4
       144 <211> LENGTH: 238
       145 <212> TYPE: PRT
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```
146 <213> ORGANISM: Canis sp.
147 <400> SEQUENCE: 4
148      Ile Val Pro Pro Asp Asp Arg Arg Gln Asn Arg Ser Phe Glu Val Met
149      1               5                   10                  15
150      Val Ala Ala Ala Leu Arg Ala Gly Arg Ala Leu Arg Gly Leu Gln Cys
151                  20                  25                  30
152      Leu Glu Leu Ala Gly Asn Arg Phe Leu Tyr Leu Pro Arg Asp Val Leu
153              35                  40                  45
154      Ala Gln Leu Pro Gly Leu Arg His Leu Asp Leu Arg Asn Asn Ser Leu
155          50                  55                  60
156      Val Ser Leu Thr Tyr Val Ser Phe Arg Asn Leu Thr His Leu Glu Ser
157      65                  70                  75                  80
158      Leu His Leu Glu Asp Asn Ala Leu Lys Val Leu His Asn Ala Thr Leu
159                  85                  90                  95
160      Ala Glu Leu Gln Ser Leu Pro His Val Arg Val Phe Leu Asp Asn Asn
161              100                 105                 110
162      Pro Trp Val Cys Asp Cys His Met Ala Asp Met Val Ala Trp Leu Lys
163              115                 120                 125
164      Glu Thr Glu Val Val Pro Gly Lys Ala Gly Leu Thr Cys Ala Phe Pro
165          130                 135                 140
166      Glu Lys Met Arg Asn Arg Ala Leu Leu Glu Leu Asn Ser Ser His Leu
167      145                 150                 155                 160
168      Asp Cys Asp Pro Ile Leu Pro Pro Ser Leu Gln Thr Ser Tyr Val Phe
169                  165                 170                 175
170      Leu Gly Ile Val Leu Ala Leu Ile Gly Ala Ile Phe Leu Leu Val Leu
171                  180                 185                 190
172      Tyr Leu Asn Arg Lys Gly Ile Lys Lys Trp Met His Asn Ile Arg Asp
173              195                 200                 205
174      Ala Cys Arg Asp His Met Glu Gly Tyr His Tyr Arg Tyr Glu Ile Asn
175          210                 215                 220
176      Ala Asp Pro Arg Leu Thr Asn Leu Ser Ser Asn Ser Asp Val
177      225                 230                 235
179 <210> SEQ ID NO: 5
180 <211> LENGTH: 9
181 <212> TYPE: PRT
182 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <223> OTHER INFORMATION: Description of Artificial Sequence: 5T4 9 Mer
185 <400> SEQUENCE: 5
186      Phe Leu Thr Gly Asn Gln Leu Ala Val
187      1               5
189 <210> SEQ ID NO: 6
190 <211> LENGTH: 9
191 <212> TYPE: PRT
192 <213> ORGANISM: Artificial Sequence
193 <220> FEATURE:
194 <223> OTHER INFORMATION: Description of Artificial Sequence: 5T4 9 Mer
195 <400> SEQUENCE: 6
196      Ala Leu Ile Gly Ala Ile Phe Leu Leu
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```
197         1                5
199 <210> SEQ ID NO: 7
200 <211> LENGTH: 9
201 <212> TYPE: PRT
202 <213> ORGANISM: Artificial Sequence
203 <220> FEATURE:
204 <223> OTHER INFORMATION: Description of Artificial Sequence: 5T4 9 Mer
205 <400> SEQUENCE: 7
206         Ser Leu Gln Thr Ser Tyr Val Phe Leu
207         1                5
209 <210> SEQ ID NO: 8
210 <211> LENGTH: 9
211 <212> TYPE: PRT
212 <213> ORGANISM: Artificial Sequence
213 <220> FEATURE:
214 <223> OTHER INFORMATION: Description of Artificial Sequence: 5T4 9 Mer
215 <400> SEQUENCE: 8
216         Ala Ile Phe Leu Leu Val Leu Tyr Leu
217         1                5
219 <210> SEQ ID NO: 9
220 <211> LENGTH: 9
221 <212> TYPE: PRT
222 <213> ORGANISM: Artificial Sequence
223 <220> FEATURE:
224 <223> OTHER INFORMATION: Description of Artificial Sequence: 5T4 9 Mer
225 <400> SEQUENCE: 9
226         Gly Leu Pro His Ile Arg Val Phe Leu
227         1                5
229 <210> SEQ ID NO: 10
230 <211> LENGTH: 9
231 <212> TYPE: PRT
232 <213> ORGANISM: Artificial Sequence
233 <220> FEATURE:
234 <223> OTHER INFORMATION: Description of Artificial Sequence: 5T4 9 Mer
235 <400> SEQUENCE: 10
236         Phe Leu Gly Ile Val Leu Ala Leu Ile
237         1                5
239 <210> SEQ ID NO: 11
240 <211> LENGTH: 9
241 <212> TYPE: PRT
242 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
244 <223> OTHER INFORMATION: Description of Artificial Sequence: 5T4 9 Mer
245 <400> SEQUENCE: 11
246         Asn Leu Thr Glu Val Pro Thr Asp Leu
247         1                5
249 <210> SEQ ID NO: 12
250 <211> LENGTH: 9
251 <212> TYPE: PRT
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 09/16/2004
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<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 66,145,277,278,287,353,358,428,429,577,580,719,788,863,868
Seq#:3; N Pos. 871

VERIFICATION SUMMARY   DATE: 09/16/2004
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Input Set : **N:\Crf3\RULE60\10774176.raw**
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```
L:89 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:92 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:95 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:98 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:101 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:104 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:107 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:110 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:113 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:116 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:119 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:122 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:125 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:127 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:60
M:341 Repeated in SeqNo=3
```